Comparison of Mouse and Human TNF Family Related Proteins (TFRPs)

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50 SQRRRGRRGE	100 AQEELVAEED SQEELTAEDR	150 AIAAHYEVHP AIAAHYEVHP	200 TRAGLYYLYC IRA <u>GLYYLYC</u>	250 QLRLCQVSGL QLRLCQVSGL	FIG. 1
QPPAPMAARR	Sraslsaqep Swatlsaqep	PKGRKTRARR PKGWKARPRR	YNRQIGEFIV YDRQIGELTV	Sataasslgp Sataasspgp	284 FQVH FQVH
SRDGGAVRQA	GLLLAVVSLG	nrlvrprrsa Eqlvrprrsa	arinsssplr tkinsssplr	VLALRCLEEF VLALRCLEEF	aapfltyfgl aapfltyfgl
RRLPLPRSLG	LGLGLALACL	EESQDPAPFL EESQDVVPFL	VDGTVSGWEE VDGTVSGWEE	YLKLDLLVDG YLKLDLLVNG	IRTLPWAHLK IRTLPWAHLK
1 MSLLDFEISA	51 PGTALLVPLA	101 QDPSELNPQT REPPELNPQT	151 RPGQDGAQAG RPGQDGAQAG	201 QVHFDEGKAV QVHFDEGKAV	251 LALRPGSSLR LPLRPGSSLR
human mouse	human mouse	human mouse	human mouse	human mouse	human mouse

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Sequence Comparison of Human Ligands in the TNF Family

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tion, time, There World wants group 30.

sequences and the disulfide linked cysteines in TNF are marked with dots. Starred sequences are motifs useful in regions between some family members, many alternative alignments can be proposed varying in the details. The bars over the sequences indicate beta strand structures in TNF and LT with the nomenclature being that used by intracellular N-terminal domains and the stalk regions spacing the C-terminal receptor binding domain from the truncated. The alignment weighs cysteine conservation heavily and due to the very poor homology in certain transmembrane region(beginning just before the first beta strand). The N terminus of human FasL has been An alignment of 10 human members of the TNF ligand family illustrating the variations in the length of the Eck and Sprang. Canonical N-linked glycosylation sites are underlined as are probable transmembrane the recognition of TNF family members.

MSTESMIRDVELAEEALPKKTGGPQGSRRC <u>IFISLFSFLIVAGATTLFCIL</u> HFGVIGPQREEFPRDLSLI MTPPERLFLPRVCGTTLHLLLGLLLVLLPGAOGLPGVGLTPSAAQTARQHPKMHLAH	MGALGLEGRGGRLQGRGSLLLAVAGATSLVTLLLAVPITVLAVLALVPQDQGGLVTETADPGAQAQ	heaslappgtvlpcptsvprrpgorrppppppppppppppppppppppppppppppp	MSLLDFEISARRLPLPRSLGSRDGGAVRQAQPPAPMAARRSQRRRGRRGEPGTA <u>LLVPLALGLGLALACIGLLLAVVSLG</u> SRASLSAQEPAEELVAEE	MAMMEVQGGPSLGQTCVLIVIFTVLLOSLCVAVTYYYFTNELKQMQDKYSKSGLAC	MPEEGSGCSVRRRPYGCVLRAALVPLVAGLVICLVVCIQRFAQAQQQLPLESLG	MDPGLQQALNGMAPPGDTAMHVPAGSVASHLGTTSRSYFYLTTAT <u>LALCLVFTVATIMVLVV</u> QRTDSIPNSPDNVPLKGG	MIETYNQTSPRSAATGLPISMKIFMYLLTVFLITOMIGSALFAVYLHRRLDKIEDERNLHEDFV	MEYASDASLDPEAPWPPAPRARACR <u>VLPWALVAGLLLLLAAACVPAVFLA</u> CPWAVSGARASPSGSAAS
hTNF hLT-α	hLT-β	hFasL	hTFRP	hTRAIL	hcD27L	hCD30L	hCD40L	h4-1BBL

FIG. 2

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hTNP	SSPLAQAVRSSSRTP
hLT-α	LITTETTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
hLT-8	OGLGFOKLPEBEPETDLS
hPast	MHTASSLEKOIGHPSPPPEKK
h4989	~
hrpatt.	PIKENDSYMDENDERSMISECHOVKWOLROLVRKMILRTSEETISTVOEKOONISPLVRERGEORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESS
15.CH24	. INTEREST OF THE PROPERTY OF
1,502,15 hCD30L	
hCD401.	ריז
h4-1BBT	PRINCESSET, SPINDAGT, I.D., ROCKLEAVISD PRINCESSET, SPINDAGT, I.D. PAOLVAQIVILIDGPLEAVISD

	A" B' B C
hTNF	RANALLAN-GVELRDNO-LVVPSEGLYLIY-SQVLFKGQGCPSTHVLLTHTISRLAVSYQTKVNLLSAIKSPCQRETPEGAEAK
hLT-a	TDRAFLOD-GFSLSNNS-LLVPTSGIYFVYNSQVVFSGKAY-SPKAT-SSPLYLAHEVQLFSSQYPFHVPLLSSQKKVY-PGLQE
hLT-8	KEQAFLT-SGTQFSDAEGLALPQDGLYYLYTCLVGYRGRAPPGGGDPQGRSVTLRSSLYRAGGAYGPGTPELLLEGAETVTPVLDPARRQGYG
hFasL	YGIVLLSGVKYKK-GGLVINETGLYFVY-SKVYFRGQSCNNQPLSHKVYMRNSKYPQDLVMMEGKMMSYCTTGQ
hTFRP	rinsssplrynroigepivtraglyyly-cqvhpdegkavylkldllvdgvlalrcleefsataasslgpqlrlcqvsgll
hTRAIL	rschsflsnihlrngelvihekgfyyiy-sqtyfrpqeeikentkndkqwqyiykytsypdpillmksarnscwskdaey
hCD27L	PALGRSFLHGPEL-DKGQLRIHRDGIYMVHI-QVTLAICSSTTASRHHPTTLAVGICSPASRSISLLRLSFHQGCTIV
hCD30L	GILHGVRYQD-GNLVIQFPGLYFII-CQLQFLVQ-CPNNSVDLKLELLINKHIKKQALVTVCESGMQTKHVYQNLSQFL
hCD40L	GYYTMSINILVTLENGKQ-LTVKRQGLYYIYA-QVTFCSINREASSQAPFIASLCLKSPGRFERILLRAAN-THSSAKPCGQQSIH
h4-188L	DGAGSSYLSQGLRYEEDKKELVVDSPGLYYVFLELKLSPTFTNTGHKVQGWVSLVLQAKPQVDDFDNLALTVELF-PCSMENKLVDRS-

H	LDFAESGQVYFGIIAL	ILVLSPSTVFFGAFAL	ndpargkt-ffganng	-SLVNFEESQT-FFGLYKL	T-YFGLFQVH	IDMDHEAS-FFGAFLVG	ET-FFGVQWVRP	E-NVLS-IFLYSNSD	vshgtgfts-fgllkl	wsqllllkaghrlsvglraylhgaqdayrdwelsyp <u>ntt</u> s-fglflvkpdnpwe
D)	P-WYEPIYLGGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL	P-WLHSMYHGAAFQLTQGDQLSTHTDGIPHLVLSPSTVFFGAFAL	PLWYTSVGFGGLVQLRRGERVYV <u>NIS</u> HPDMVDPARGKT-FFGAVMVG	-MWARSSYLGAVFNLTSADHLYVNVSELSLVNFEESQT-FFGLYKL	alrpgsslrirtlpwahlkaapfl	GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFGAFLVG	-SORLTPLARGDILCTMLIGILLPSR-NTDET-FFGVQWVRP	LDYLQVNITISVNVDTFQYIDTST-FPLE-NVLS-IFLYSNSD	LGGVFELQPGASVFVNVTDPSQVSHGTGFTS-FGLLKL	llkaghrlsvglraylhgaqday.
į	P-WYEPI	P-WLHSM	PLWYTSV	-MWARSS	ALRPGSS	GLYSI	-SORLTP	LDYLQ	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	WSQLL
	hTNF	hLT-α	hLT-B	hFasL	htprp	htrail	hCD27L	hCD30L	hCD40L	h4-1BBL

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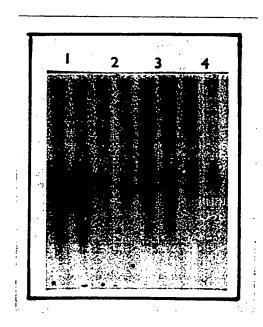


FIG. 3

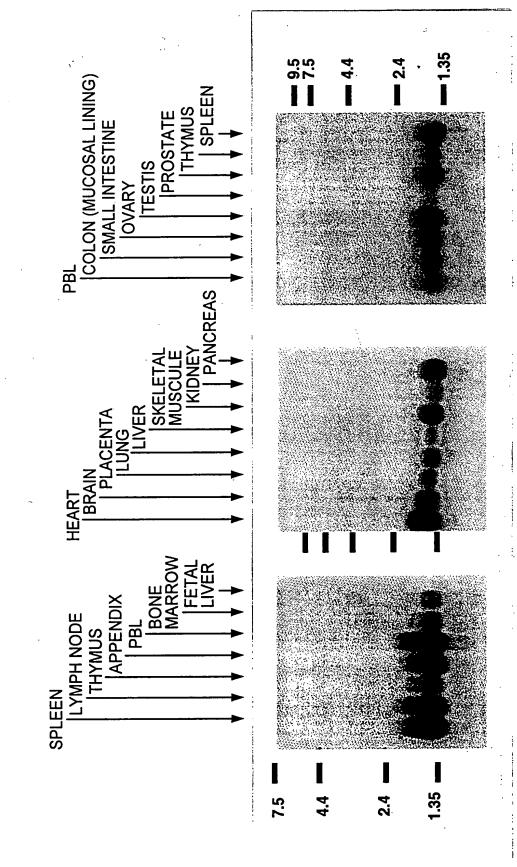


FIG. 4

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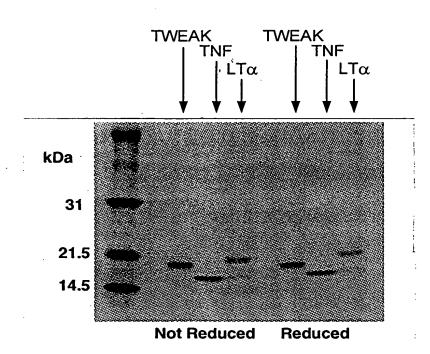


FIG. 5



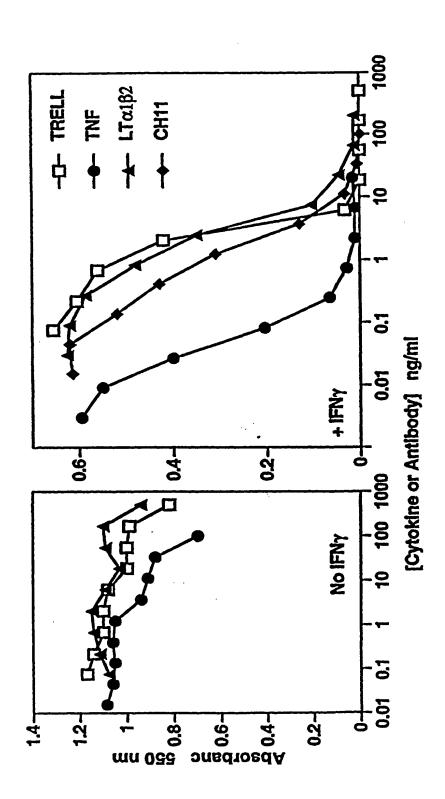


FIG. 6A

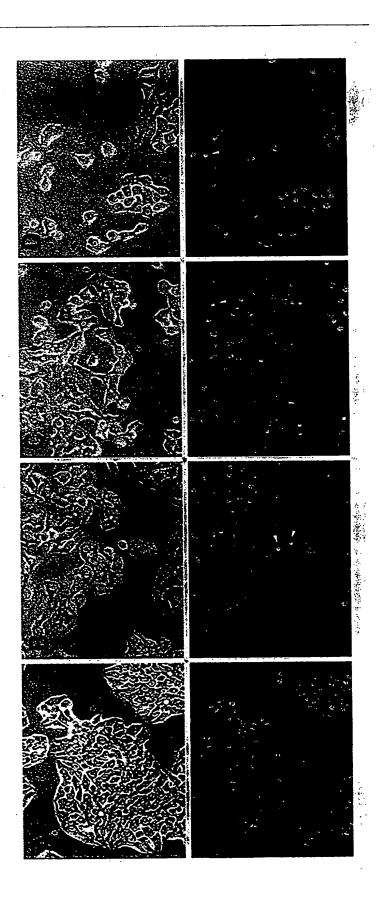


FIG. 6B